



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:16 AM UTC

PDB ID : 5KST / pdb_00005kst
Title : Stationary phase Survival protein E (SurE) from Xylella fastidiosa- XfSurE-TSamp (Tetramer Smaller - crystallization with 3'AMP).
Authors : Machado, A.T.P.; Fonseca, E.M.B.; Dos Reis, M.A.; Saraiva, A.M.; Dos Santos, C.A.; De Toledo, M.A.S.; Polikarpov, I.; De Souza, A.P.; Aparicio, R.; Iulek, J.
Deposited on : 2016-07-09
Resolution : 2.76 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

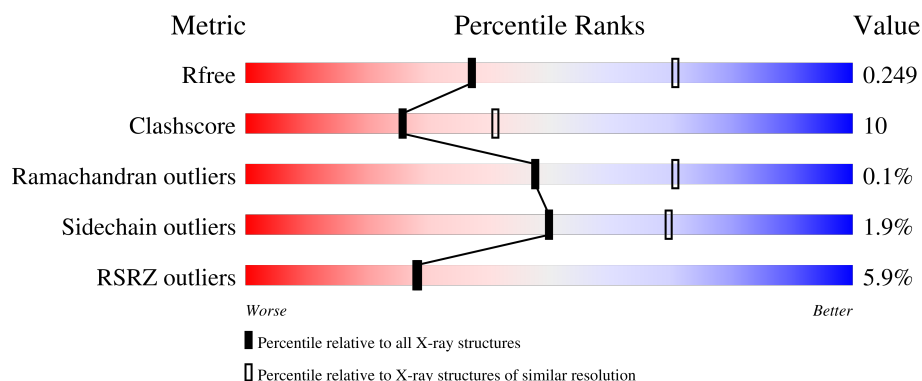
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	270	 4% 76% 17% • 5%
1	B	270	 7% 78% 16% • 5%
1	C	270	 3% 71% 22% • 6%
1	D	270	 9% 73% 21% • 6%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	IOD	C	502	-	-	X	-
3	IOD	D	603	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8043 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 5'-nucleotidase SurE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	61	1	0
			1953	1216	348	381	8			
1	B	257	Total	C	N	O	S	23	6	0
			1994	1240	358	387	9			
1	C	254	Total	C	N	O	S	36	0	0
			1930	1203	347	373	7			
1	D	255	Total	C	N	O	S	66	0	0
			1937	1207	347	375	8			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	263	LEU	-	expression tag	UNP Q9PF20
A	264	GLU	-	expression tag	UNP Q9PF20
A	265	HIS	-	expression tag	UNP Q9PF20
A	266	HIS	-	expression tag	UNP Q9PF20
A	267	HIS	-	expression tag	UNP Q9PF20
A	268	HIS	-	expression tag	UNP Q9PF20
A	269	HIS	-	expression tag	UNP Q9PF20
A	270	HIS	-	expression tag	UNP Q9PF20
B	263	LEU	-	expression tag	UNP Q9PF20
B	264	GLU	-	expression tag	UNP Q9PF20
B	265	HIS	-	expression tag	UNP Q9PF20
B	266	HIS	-	expression tag	UNP Q9PF20
B	267	HIS	-	expression tag	UNP Q9PF20
B	268	HIS	-	expression tag	UNP Q9PF20
B	269	HIS	-	expression tag	UNP Q9PF20
B	270	HIS	-	expression tag	UNP Q9PF20
C	263	LEU	-	expression tag	UNP Q9PF20
C	264	GLU	-	expression tag	UNP Q9PF20
C	265	HIS	-	expression tag	UNP Q9PF20
C	266	HIS	-	expression tag	UNP Q9PF20
C	267	HIS	-	expression tag	UNP Q9PF20

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Chain	Residue	Modelled	Actual	Comment	Reference
C	268	HIS	-	expression tag	UNP Q9PF20
C	269	HIS	-	expression tag	UNP Q9PF20
C	270	HIS	-	expression tag	UNP Q9PF20
D	263	LEU	-	expression tag	UNP Q9PF20
D	264	GLU	-	expression tag	UNP Q9PF20
D	265	HIS	-	expression tag	UNP Q9PF20
D	266	HIS	-	expression tag	UNP Q9PF20
D	267	HIS	-	expression tag	UNP Q9PF20
D	268	HIS	-	expression tag	UNP Q9PF20
D	269	HIS	-	expression tag	UNP Q9PF20
D	270	HIS	-	expression tag	UNP Q9PF20

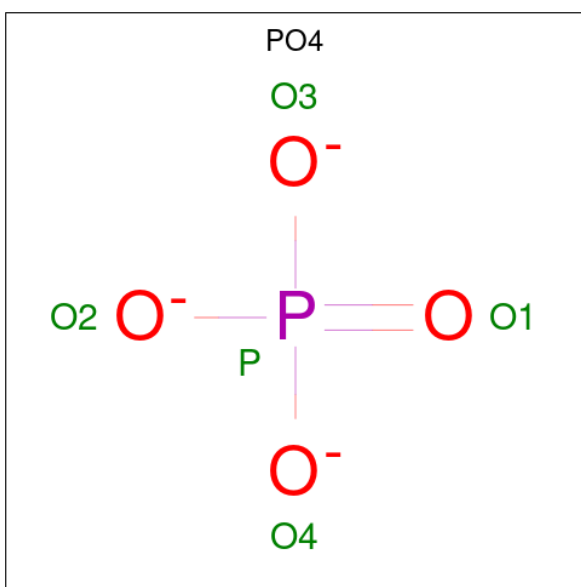
- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mn 1 1	0	0
2	B	1	Total Mn 1 1	0	0
2	C	1	Total Mn 1 1	0	0
2	D	1	Total Mn 1 1	0	0

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total I 2 2	0	0
3	B	1	Total I 1 1	0	0
3	C	1	Total I 1 1	0	0
3	D	2	Total I 2 2	0	0

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	C	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is water.

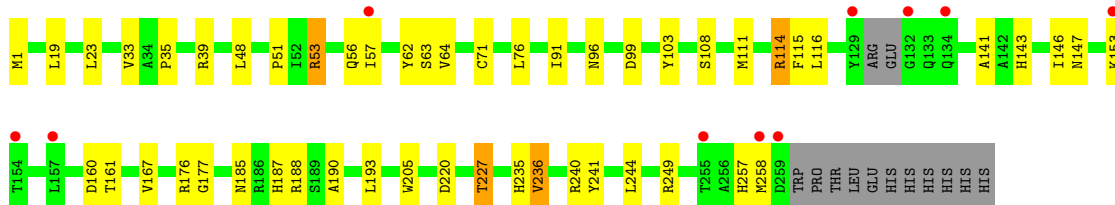
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	50	Total	O	0	0
			50	50		
5	B	56	Total	O	0	1
			57	57		
5	C	55	Total	O	0	0
			55	55		
5	D	37	Total	O	0	0
			37	37		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

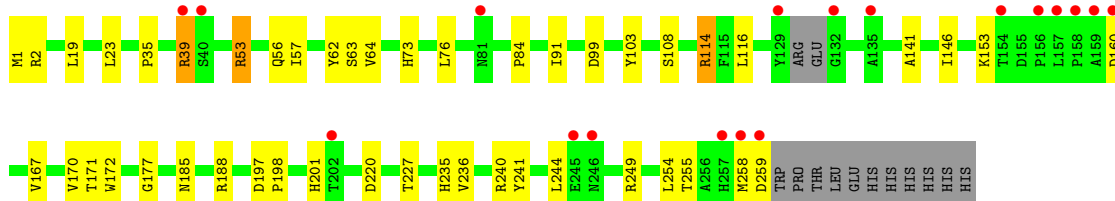
• Molecule 1: 5'-nucleotidase SurE

Chain A: 



• Molecule 1: 5'-nucleotidase SurE

Chain B: 



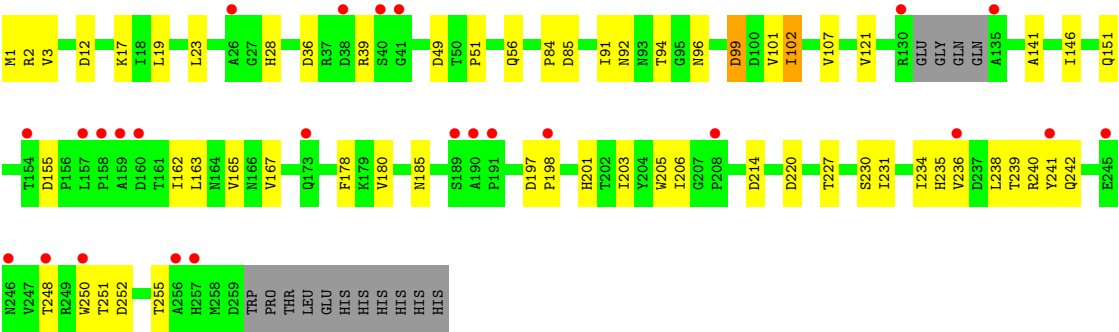
• Molecule 1: 5'-nucleotidase SurE

Chain C: 



• Molecule 1: 5'-nucleotidase SurE

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.00Å 78.21Å 82.16Å 90.00° 96.74° 90.00°	Depositor
Resolution (Å)	77.96 – 2.76 77.96 – 2.76	Depositor EDS
% Data completeness (in resolution range)	97.5 (77.96-2.76) 97.4 (77.96-2.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.12 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.197 , 0.248 0.198 , 0.249	Depositor DCC
R_{free} test set	1255 reflections (1.37%)	wwPDB-VP
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.438	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8043	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.29% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, IOD, PO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.39	0/1995	0.84	9/2731 (0.3%)
1	B	0.38	0/2036	0.82	9/2784 (0.3%)
1	C	0.37	0/1969	0.73	0/2696
1	D	0.36	0/1976	0.75	1/2705 (0.0%)
All	All	0.38	0/7976	0.79	19/10916 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	ARG	NE-CZ-NH2	7.76	126.19	119.20
1	A	53	ARG	NE-CZ-NH2	7.58	126.02	119.20
1	B	39	ARG	NE-CZ-NH2	7.53	125.98	119.20
1	B	39	ARG	NE-CZ-NH1	-7.26	114.24	121.50
1	A	249	ARG	NE-CZ-NH1	-7.24	114.26	121.50
1	D	236	VAL	N-CA-C	-7.13	106.13	112.12
1	A	53	ARG	NE-CZ-NH1	-7.09	114.41	121.50
1	A	236	VAL	N-CA-C	-6.99	105.24	113.42
1	B	53	ARG	CD-NE-CZ	6.04	132.86	124.40
1	B	53	ARG	NE-CZ-NH2	-5.91	113.88	119.20
1	A	249	ARG	CD-NE-CZ	5.72	132.40	124.40
1	B	236	VAL	N-CA-C	-5.69	106.76	113.42
1	A	39	ARG	CD-NE-CZ	5.59	132.22	124.40
1	A	39	ARG	NE-CZ-NH2	-5.56	114.20	119.20
1	B	249	ARG	NE-CZ-NH2	-5.54	114.21	119.20
1	B	249	ARG	CD-NE-CZ	5.51	132.11	124.40
1	B	39	ARG	CD-NE-CZ	5.28	131.79	124.40
1	A	53	ARG	CD-NE-CZ	5.20	131.68	124.40
1	B	53	ARG	NE-CZ-NH1	5.19	126.69	121.50

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1953	0	1919	42	0
1	B	1994	0	1961	37	0
1	C	1930	0	1904	57	0
1	D	1937	0	1909	52	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	2	0	0	0	0
3	B	1	0	0	1	0
3	C	1	0	0	3	0
3	D	2	0	0	3	0
4	A	5	0	0	1	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	1	0
5	A	50	0	0	2	0
5	B	57	0	0	2	0
5	C	55	0	0	5	0
5	D	37	0	0	0	0
All	All	8043	0	7693	144	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (144) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:242:GLN:NE2	3:C:502:IOD:I	2.89	0.75
1:B:39:ARG:NH1	5:B:401:HOH:O	2.19	0.74
1:A:176:ARG:HG3	1:A:227:THR:HB	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:HIS:CD2	1:D:206:ILE:HD12	2.29	0.67
1:B:53:ARG:NH1	1:C:49:ASP:O	2.28	0.67
1:B:57:ILE:HD11	1:B:63:SER:HB2	1.78	0.66
1:A:57:ILE:HD11	1:A:63:SER:HB2	1.77	0.65
1:D:242:GLN:HG3	3:D:603:IOD:I	2.68	0.64
1:C:186:ARG:NH1	5:C:604:HOH:O	2.22	0.64
1:A:188:ARG:HA	1:B:116:LEU:HD22	1.80	0.64
1:C:99:ASP:OD1	5:C:601:HOH:O	2.15	0.64
1:D:101:VAL:HG13	1:D:107:VAL:HG21	1.80	0.63
1:C:101:VAL:HG13	1:C:107:VAL:HG21	1.80	0.62
1:D:96:ASN:ND2	4:D:604:PO4:O4	2.20	0.62
1:B:2:ARG:HB3	1:B:84:PRO:HA	1.82	0.62
1:A:91:ILE:O	5:A:601:HOH:O	2.17	0.60
1:A:257:HIS:NE2	1:B:177:GLY:HA2	2.15	0.60
1:C:253:ARG:NE	1:D:155:ASP:OD2	2.34	0.60
1:A:177:GLY:HA3	1:B:255[B]:THR:HG23	1.82	0.60
1:C:248:THR:HA	1:D:180:VAL:HG21	1.84	0.59
1:A:116:LEU:HD22	1:B:188:ARG:HA	1.84	0.59
1:A:115:PHE:CE1	1:A:236:VAL:HG12	2.38	0.58
1:B:1:MET:HE1	1:B:153:LYS:HB2	1.85	0.58
1:C:203:ILE:HB	1:D:51:PRO:HB2	1.85	0.58
1:A:257:HIS:CE1	1:B:177:GLY:HA2	2.38	0.58
1:A:1:MET:HE1	1:A:153:LYS:HB2	1.85	0.57
1:C:23:LEU:HD23	1:C:146:ILE:HG22	1.86	0.57
1:C:242:GLN:CD	3:C:502:IOD:I	3.17	0.57
1:C:242:GLN:OE1	3:C:502:IOD:I	2.93	0.57
1:D:23:LEU:HD23	1:D:146:ILE:HG22	1.86	0.56
1:C:180:VAL:HG21	1:D:248:THR:HA	1.86	0.56
1:D:185:ASN:HB2	1:D:214:ASP:HB3	1.88	0.56
1:D:241:TYR:N	3:D:603:IOD:I	3.10	0.55
1:A:48:LEU:O	1:C:199:ARG:NH1	2.39	0.55
1:A:141:ALA:HA	1:A:167:VAL:HG21	1.89	0.55
1:B:114:ARG:HD2	1:B:160:ASP:HA	1.88	0.55
1:C:148:ILE:HG23	1:D:250:TRP:CH2	2.42	0.55
1:C:36:ASP:OD1	1:C:39:ARG:NH1	2.25	0.54
1:B:141:ALA:HA	1:B:167:VAL:HG21	1.89	0.54
1:D:99:ASP:OD1	1:D:99:ASP:N	2.37	0.54
1:D:12:ASP:HA	1:D:17:LYS:HE3	1.89	0.54
1:C:238:LEU:HD11	1:D:102:ILE:HD12	1.90	0.54
1:A:53:ARG:HH11	1:D:49:ASP:HA	1.74	0.53
1:A:19:LEU:HB2	1:A:91:ILE:HG13	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:PRO:HB2	1:D:203:ILE:HB	1.91	0.53
1:C:12:ASP:HA	1:C:17:LYS:HE3	1.89	0.53
1:C:240:ARG:HD2	1:D:235:HIS:CE1	2.44	0.52
1:B:19:LEU:HB2	1:B:91:ILE:HG13	1.92	0.52
1:B:198:PRO:HB2	1:C:208:PRO:HD3	1.92	0.51
1:A:143:HIS:NE2	1:B:259[B]:ASP:O	2.44	0.50
1:B:254:LEU:HD23	1:B:258[B]:MET:HG3	1.94	0.49
1:C:247:VAL:HA	1:C:250:TRP:HB3	1.95	0.49
1:C:205:TRP:CH2	1:D:51:PRO:HD3	2.48	0.49
1:D:92:ASN:ND2	1:D:94:THR:O	2.46	0.48
1:A:114:ARG:HD2	1:A:160:ASP:HA	1.95	0.48
1:C:222:ASP:OD2	5:C:602:HOH:O	2.19	0.48
1:A:51:PRO:HD2	1:D:51:PRO:HD2	1.93	0.48
1:A:185:ASN:HB3	5:A:602:HOH:O	2.14	0.48
1:A:187:HIS:O	1:B:73:HIS:HE1	1.96	0.48
1:C:162:ILE:HD11	1:C:234:ILE:HD11	1.96	0.48
1:D:162:ILE:HD11	1:D:234:ILE:HD11	1.95	0.48
1:C:3:VAL:HG11	1:C:23:LEU:HD13	1.96	0.47
1:D:91:ILE:HD13	1:D:141:ALA:HB3	1.95	0.47
1:D:19:LEU:HB2	1:D:91:ILE:HG13	1.97	0.47
1:C:238:LEU:O	1:D:235:HIS:N	2.33	0.47
1:D:121:VAL:HG22	1:D:163:LEU:HB2	1.97	0.47
1:A:96:ASN:ND2	4:A:503:PO4:O4	2.36	0.47
1:C:19:LEU:HB2	1:C:91:ILE:HG13	1.95	0.47
1:B:91:ILE:HD13	1:B:141:ALA:HB3	1.97	0.46
1:C:51:PRO:HD3	1:D:205:TRP:CH2	2.51	0.46
1:C:91:ILE:HD13	1:C:141:ALA:HB3	1.97	0.46
1:D:2:ARG:HB2	1:D:84:PRO:HA	1.98	0.46
1:A:193:LEU:HD12	1:D:198:PRO:HB3	1.98	0.46
1:A:205:TRP:CG	1:D:198:PRO:HG2	2.51	0.46
1:C:121:VAL:HG22	1:C:163:LEU:HB2	1.97	0.46
1:B:185:ASN:HB3	5:B:422:HOH:O	2.16	0.46
1:C:161:THR:OG1	1:D:240:ARG:NH2	2.44	0.46
1:A:76:LEU:HD12	1:A:116:LEU:HD12	1.97	0.46
1:D:3:VAL:HG11	1:D:23:LEU:HD13	1.97	0.45
1:C:2:ARG:HB2	1:C:84:PRO:HA	1.98	0.45
1:C:254:LEU:HB2	1:D:151:GLN:HG2	1.96	0.45
1:D:242:GLN:N	3:D:603:IOD:I	3.09	0.45
1:C:128:LEU:HB2	1:C:130:ARG:HD2	1.99	0.45
1:A:56:GLN:HG3	1:A:62:TYR:CZ	2.52	0.45
1:B:241:TYR:HA	1:B:244:LEU:HG	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:178:PHE:HD2	1:C:231:ILE:HD11	1.82	0.45
1:A:114:ARG:HH11	1:A:161:THR:H	1.63	0.45
1:B:220:ASP:N	1:B:220:ASP:OD1	2.49	0.44
1:A:241:TYR:HA	1:A:244:LEU:HG	2.00	0.44
1:A:51:PRO:CD	1:D:51:PRO:HD2	2.48	0.44
1:B:56:GLN:HG3	1:B:62:TYR:CZ	2.53	0.44
1:C:205:TRP:CZ2	1:D:51:PRO:HD3	2.52	0.44
1:A:91:ILE:HD13	1:A:141:ALA:HB3	1.99	0.44
1:D:1:MET:HE3	1:D:85:ASP:HB2	2.00	0.44
1:A:220:ASP:N	1:A:220:ASP:OD1	2.49	0.44
1:A:103:TYR:OH	1:B:108:SER:HA	2.18	0.44
1:A:23:LEU:HD23	1:A:146:ILE:HG22	2.00	0.43
1:C:1:MET:HG2	1:C:28:HIS:ND1	2.33	0.43
1:C:92:ASN:ND2	1:C:94:THR:O	2.50	0.43
1:D:220:ASP:N	1:D:220:ASP:OD1	2.51	0.43
1:D:1:MET:HG2	1:D:28:HIS:ND1	2.33	0.43
1:A:205:TRP:CD2	1:D:198:PRO:HD2	2.53	0.43
1:B:76:LEU:HD12	1:B:116:LEU:HD12	1.99	0.43
1:C:148:ILE:HG23	1:D:250:TRP:HH2	1.82	0.43
1:A:108:SER:HA	1:B:103:TYR:OH	2.17	0.43
1:B:23:LEU:HD23	1:B:146:ILE:HG22	2.01	0.43
1:D:178:PHE:HD2	1:D:231:ILE:HD11	1.83	0.43
1:C:1:MET:HE3	1:C:85:ASP:HB2	2.01	0.43
1:C:146:ILE:O	5:C:603:HOH:O	2.21	0.43
1:C:102:ILE:HD12	1:D:238:LEU:HD11	2.00	0.43
1:C:197:ASP:HB3	1:C:203:ILE:HD13	2.01	0.43
1:C:220:ASP:OD1	1:C:220:ASP:N	2.51	0.43
1:B:235:HIS:CE1	3:B:301:IOD:I	3.42	0.42
1:A:235:HIS:CE1	1:B:240:ARG:HD2	2.55	0.42
1:B:35:PRO:HA	1:B:64:VAL:O	2.19	0.42
1:D:197:ASP:HB3	1:D:203:ILE:HD13	2.01	0.42
1:A:240:ARG:HD2	1:B:235:HIS:CE1	2.54	0.42
1:B:170:VAL:HG23	1:B:171:THR:O	2.19	0.42
1:A:147:ASN:HD21	1:B:259[B]:ASP:HB3	1.83	0.42
1:A:257:HIS:HB3	1:B:172:TRP:HE1	1.85	0.42
1:C:251:THR:HA	1:C:254:LEU:HB3	2.02	0.42
1:A:190:ALA:O	1:B:73:HIS:NE2	2.53	0.42
1:C:185:ASN:HB3	1:C:214:ASP:HB3	2.02	0.42
1:C:197:ASP:OD1	1:C:201:HIS:N	2.53	0.42
1:A:35:PRO:HA	1:A:64:VAL:O	2.20	0.41
1:D:252:ASP:HA	1:D:255:THR:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:239:THR:HB	1:C:241:TYR:CE1	2.55	0.41
1:D:36:ASP:OD1	1:D:39:ARG:NH1	2.46	0.41
1:C:12:ASP:HB2	5:C:630:HOH:O	2.20	0.41
1:C:114:ARG:HG2	1:C:236:VAL:HG21	2.02	0.41
1:D:141:ALA:HA	1:D:167:VAL:HG21	2.02	0.41
1:B:198:PRO:HB3	1:C:193:LEU:HD12	2.03	0.41
1:C:51:PRO:HB3	1:D:205:TRP:CE2	2.55	0.41
1:B:201:HIS:CE1	1:C:129:TYR:HB2	2.55	0.41
1:A:33:VAL:HG12	1:A:71:CYS:HB3	2.02	0.41
1:B:197:ASP:HB2	1:B:198:PRO:HD2	2.02	0.41
1:C:231:ILE:HD13	1:D:250:TRP:HZ3	1.86	0.41
1:D:197:ASP:OD1	1:D:201:HIS:N	2.54	0.41
1:D:165:VAL:HA	1:D:230:SER:O	2.20	0.41
1:A:111:MET:SD	1:A:236:VAL:HG13	2.61	0.40
1:C:114:ARG:HD2	1:C:114:ARG:HA	1.81	0.40
1:D:239:THR:HB	1:D:241:TYR:CE1	2.56	0.40
1:C:247:VAL:O	1:C:251:THR:N	2.52	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	254/270 (94%)	245 (96%)	8 (3%)	1 (0%)	30	50
1	B	258/270 (96%)	245 (95%)	13 (5%)	0	100	100
1	C	250/270 (93%)	239 (96%)	11 (4%)	0	100	100
1	D	251/270 (93%)	239 (95%)	12 (5%)	0	100	100
All	All	1013/1080 (94%)	968 (96%)	44 (4%)	1 (0%)	48	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	258	MET

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	212/224 (95%)	210 (99%)	2 (1%)	70	82
1	B	216/224 (96%)	213 (99%)	3 (1%)	59	75
1	C	209/224 (93%)	203 (97%)	6 (3%)	37	61
1	D	210/224 (94%)	205 (98%)	5 (2%)	43	65
All	All	847/896 (94%)	831 (98%)	16 (2%)	50	70

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	ARG
1	A	227	THR
1	B	99	ASP
1	B	114	ARG
1	B	227	THR
1	C	56	GLN
1	C	99	ASP
1	C	102	ILE
1	C	128	LEU
1	C	227	THR
1	C	236	VAL
1	D	56	GLN
1	D	99	ASP
1	D	102	ILE
1	D	227	THR
1	D	251	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	A	96	ASN
1	A	137	GLN
1	B	56	GLN
1	B	96	ASN
1	B	137	GLN
1	B	143	HIS
1	C	147	ASN
1	D	147	ASN
1	D	187	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 10 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	PO4	A	503	2	4,4,4	0.89	0	6,6,6	0.43	0
4	PO4	B	303	2	4,4,4	0.95	0	6,6,6	0.53	0
4	PO4	C	503	2	4,4,4	0.94	0	6,6,6	0.54	0
4	PO4	D	604	2	4,4,4	0.96	0	6,6,6	0.45	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	503	PO4	1	0
4	D	604	PO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	257/270 (95%)	0.24	10 (3%)	43 40	22, 44, 77, 119	17 (6%)
1	B	257/270 (95%)	0.32	18 (7%)	22 22	26, 43, 83, 122	11 (4%)
1	C	254/270 (94%)	0.28	7 (2%)	55 53	23, 45, 81, 101	7 (2%)
1	D	255/270 (94%)	0.73	25 (9%)	13 12	26, 55, 99, 133	17 (6%)
All	All	1023/1080 (94%)	0.39	60 (5%)	28 28	22, 47, 86, 133	52 (5%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	245	GLU	5.0
1	D	250	TRP	4.9
1	B	257[A]	HIS	4.5
1	D	130	ARG	4.1
1	D	41	GLY	3.8
1	D	157	LEU	3.8
1	D	191	PRO	3.7
1	D	158	PRO	3.5
1	B	132	GLY	3.5
1	C	173	GLN	3.3
1	D	246	ASN	3.3
1	B	160	ASP	3.3
1	D	160	ASP	3.3
1	A	129	TYR	3.2
1	B	159	ALA	3.2
1	C	185	ASN	3.2
1	B	258[A]	MET	3.2
1	A	154	THR	3.1
1	B	135	ALA	3.1
1	B	129	TYR	3.1
1	D	173	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	246	ASN	3.0
1	A	132	GLY	3.0
1	D	248	THR	2.9
1	D	208	PRO	2.8
1	C	41	GLY	2.8
1	A	157	LEU	2.8
1	D	256	ALA	2.8
1	D	198	PRO	2.7
1	D	159	ALA	2.6
1	D	190	ALA	2.6
1	D	135	ALA	2.5
1	D	236	VAL	2.5
1	A	259	ASP	2.5
1	B	259[A]	ASP	2.4
1	A	258	MET	2.4
1	D	154	THR	2.4
1	C	257	HIS	2.4
1	B	40	SER	2.4
1	B	39	ARG	2.4
1	C	160	ASP	2.3
1	D	241	TYR	2.3
1	B	154	THR	2.3
1	B	156	PRO	2.3
1	A	134	GLN	2.2
1	D	38	ASP	2.2
1	B	157	LEU	2.2
1	A	255	THR	2.2
1	B	202	THR	2.2
1	D	189	SER	2.2
1	C	42	ALA	2.2
1	D	40	SER	2.2
1	A	57	ILE	2.2
1	C	187	HIS	2.2
1	B	81	ASN	2.1
1	D	257	HIS	2.1
1	B	158	PRO	2.1
1	B	245	GLU	2.0
1	D	26	ALA	2.0
1	A	153	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	IOD	A	504	1/1	0.93	0.09	83,83,83,83	1
4	PO4	D	604	5/5	0.93	0.11	53,53,54,55	0
3	IOD	D	603	1/1	0.94	0.07	78,78,78,78	1
3	IOD	C	502	1/1	0.94	0.09	113,113,113,113	1
4	PO4	B	303	5/5	0.96	0.08	33,36,36,37	0
3	IOD	B	301	1/1	0.96	0.10	165,165,165,165	1
4	PO4	C	503	5/5	0.97	0.08	37,37,38,38	0
4	PO4	A	503	5/5	0.98	0.10	38,40,42,42	0
3	IOD	D	601	1/1	0.99	0.04	55,55,55,55	1
2	MN	D	602	1/1	0.99	0.02	49,49,49,49	0
3	IOD	A	502	1/1	0.99	0.03	49,49,49,49	1
2	MN	A	501	1/1	0.99	0.02	39,39,39,39	0
2	MN	B	302	1/1	0.99	0.02	37,37,37,37	0
2	MN	C	501	1/1	0.99	0.03	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.